

TITLE: MANGROVE SOIL BIOREMEDIATION - MICROBIAL COMMUNITIES DIVERSITY AND POTENTIAL

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ABSTRACT:

Oil spills constitute one of the worst anthropogenic impacts to the environments, and due to their ecotonal location and structural peculiarities, mangroves became one of the most threatened ecosystems by petroleum derivatives. Herein, we simulated, in an estuarine mesocosm, an occurrence of oil spill in a real mangrove ecosystem and provide information on biological hydrocarbon degradation by comparing the efficiency of four classical biorremediation strategies: Bioattenuation - BT, Bioaugmentation - BA, Biostimulation - BS, and Bioaugmentation + Biostimulation - BB. We also characterized the molecular (presence of *alkB*, *ndo*, *assA* and *bssA* genes) and ecological structure of microbial communities from mangrove soil at Restinga da Marambaia, Rio de Janeiro, Brazil. We evidenced that hydrocarbon degradation efficiency was higher at superficial soil layers, but there was no differences in terms of hydrocarbon degradation rates (TPH and alkanes) and number of the hydrocarbon-degrading genes *alkB* and *ndo* among the biorremediation treatments. Samples from the deeper stratum presented the greater number of the hydrocarbon-degrading genes analyzed, with exception of the genes *assA* and *bssA* that could not be detected in any of our samples. The diversity of bacterial communities differed among treatments and depths. We found a high bacterial diversity, with more than eleven thousand different OTUs, classified into 26 phyla and 402 genera. In all treatments and depths, the most abundant phyla were Proteobacteria, Firmicutes and Bacteroidetes, with the classes Gammaproteobacteria, Flavobacteriales and Clostridiales being the most abundant ones. Indicator specie analysis showed 26 different genera significantly associated with specific bioremediation conditions (BA =10, BS = 9, BT = 7). The deeper soil layer presented the greatest number of OTUs. Our results demonstrate the potential of bioattenuation as a long-term strategy for mangrove soil decontamination and suggest that environmental factors may select particular bacterial communities in distinct habits.

Keywords: Bioremediation, Bacterial diversity, Mangrove, Oil-degrading genes.